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Estimates of Genetic Effects of Yield and Related Traits through Generation Mean Analysis in Bread Wheat

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ABSTRACT

In order to study the gene effects for grain yield and other component traits of cross WH1105 X WH711 of wheat (Triticum aestivum L. em. Thell) five generations i.e. parents (P_1 and P_2), F_1, F_2 and F_3 were studied using generation mean analysis. The C-scaling test was significant for all the characters indicating thereby the presence of non-allelic interactions. Generation mean analysis revealed significant differences for all traits studied. Additive gene effects was significant for most of the characters and higher in magnitude over the dominance gene effects. Additive x additive (i) and dominant x dominant (l) type of interaction have been significant for most of the characters. Duplicate epistasis was recorded for number of tillers per plant, grain yield per plant and biological yield/plant.

Key words: *C-scaling test, gene effects, generation mean analysis, wheat (Triticum aestivum L. em. Thell)*

INTRODUCTION

Wheat (*Triticum aestivum* L. em. Thell) is the most important cereal crop in India and serves as the staple food crop for more than 1 billion population. India contributes approximately 14% to the world wheat basket and share 11% of wheat area[12]. Wheat belongs to the sub-tribe *Triticinae* and the tribe *Triticeae* (= *Hordeae*) within the *Poaceae* family. In India wheat was cultivated on 30.23 million ha area with a production of 96.64 million tonnes (2016-17). Area, production and productivity of Haryana was 2.54 million ha, 11.14 million tonnes and 43.90 q/ha respectively in 2016-17[1]. The main objective of wheat breeding is to increase grain yield, however, yield is a quantitative trait and is affected by many genetic and non-genetic factors. To increase yield, it is necessary to improve component traits which affect grain yield, but in order to achieve this, more information on the inheritance pattern of these traits is necessary. The genetical studies based on the mean and variance of basic generations, is a simple method for estimating gene effects for polygenic traits. Generation mean analysis estimate the epistatic effects also[3].

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The knowledge of gene action helps in the choice of appropriate breeding procedure in improvement of the yield and yield attributing traits. Thus, the present study was undertaken to study the gene effects and inheritance pattern of grain yield and other traits.

MATERIAL AND METHODS

Plant Materials and Experiments:

Two well adapted and high yielding varieties *viz;* WH1105 and WH711 of North Western Plain Zone were used to develop different generations.

Table 1: Pedigrees of wheat genotypes used in the present study

Sr. No.	GENOTYPE	SOURCE	PEDIGREE
1	WH1105	CCSHAU, Hisar	MILAN/S87230//BABAX
2	WH711	CCSHAU, Hisar	ALD'S'HUAC/HD2285/3/HFW-17

Parents, F_1, F_2 and F_3 were grown in the field during 2014-15 and 2015-16 in the research area of wheat section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Data were recorded on variation in morphological traits and agronomically superior plants were selected from the population of F_2 generation. The number of plants analyzed varied as follows: 5 plants for the homogeneous population i.e. P_1, P_2 and F_1 generation and 150 plants for the heterogeneous population (F_2 and F_3 generations). The data was recorded for the traits *viz;* plant height (cm), number of tillers per plant, spike length (cm), spike weight (g), number of grains per spike, number of spikelet per spike, 1000 grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%).

Scaling test: To predict the genetic control of traits, '*d*' and '*h*' effects were assumed to be present. The data was tested to fit in simple additive-dominance model which was tested by the C-scaling test. The quantities in C-scaling test[5] and their variances[7], standard error and 't' test were calculated for detection of digenic interactions or to fit in simple additive- dominance model using the following formulae.

Scale C = $4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \overline{P_2} = 0$

$V_C = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\overline{P_2})$

SE (C) = $(V_C)^{1/2}$

't'=C/SE(C)

Where, $\bar{P}_1$, $\overline{P_2}$, $\bar{F}_1$ and $\bar{F}_2$ are the means of different generations over replications. The variance V_C of the scale C was obtained as the square root of V_C. The significance of the deviations of the scales from zero was tested using standard error. The significance of the scale C was determined by comparing the observed and expected 't' values at 5 and 1% level of significance. The characters with significant values were further analysed by five parameter model.

Five parameter model: In this method the mean of each character is indicated as follows:

$$Y = m + C1(d) + C2(h) + C3(i) + C4(l)$$

Where,

m = mean effect

d = the sum of additive gene effect

h = the sum of dominance gene effect

i = the sum of additive x additive interaction

l = the sum of dominance x dominance interaction

C1, C2…………C4= Co-efficient for gene effects

The means of the different generations were utilized for obtaining the various genetic effects. Estimates using five parameter models of Hayman[4], Jinks and Jones[6] and further described by Singh and Panwar[11] were derived as:

$m = \bar{F}_2$

$(d) = 1/2\bar{P}_1 - 1/2\ \overline{P_2}$

$(h) = 1/6\ (4\bar{F}_1 - 12\bar{F}_2 - 16\bar{F}_3)$

$(i) = \bar{P}_1 - \bar{F}_2 + (1/2)(\bar{P}_1 - \overline{P_2} + h) - 1/4l$

$(l) = 1/3\ (16\bar{F}_3 - 24\bar{F}_2 + 8\bar{F}_1)$

RESULTS AND DISCUSSION

The means of five generations for different characters has been presented in Fig.1. The parent P_1 (WH1105) had greater plant height as compared to that of parent P_2 (WH711) for all the six traits *viz*; number of tillers per plant, spike length, spike weight, number of grains per spike, 1000 grain weight, grain yield and biological yield per plant. The mean value of F_1 was intermediate to the parents. The F_2 average was higher than that of F_1 as well as F_3 means. The C-scaling test was applied to the data to determine adequacy of the additive-dominance model for different traits. All the traits showed deviation from zero indicated that additive-dominance model was inadequate. Hence, as a result the five parameter model was used. The estimates of genetic parameters *m*, [*d*], [*h*], [*i*] and [*l*] along with their standard errors have been presented in Table 2. The present study revealed that the plant height and harvest index were governed by additive effect. The magnitude of additive gene effect was higher as compared to dominance component for most of the traits. As regards to the epistatic interactions, both kinds of interactions i.e. additive x additive and dominant x dominant effects were observed. There was no evidence of epistatic effect which indicated the presence of higher order interaction i.e. trigenic interaction and linkage in this trait. Additive effect for plant height were also reported by Shekhawat *et al.*[10] and Dobariya *et al.*[2] and many others. In case of number of tillers per plant, grain yield and biological yield per plant, both additive and dominance gene effects were significant, but the magnitude of additive effect was higher than the dominance component. The sign of *h* and *l* were opposite which showed duplicate type of epistasis. These findings are in agreement with the findings of Dobariya *et al.*[2]; Mohamed[8] and Said[9] and Yadav et *al.*[13].The characters *viz;* spike length, number of grains per spike, number of spikelets per spike and 1000 grain weight, were governed by additive gene effect while dominance component was comparatively lower than the additive component. Thus, due to the predominant role of additive effect selection in early generation will be effective for these traits. Additive x additive and dominance x dominance gene interactions were also observed for most of the traits. Dobariya *et al.*[2] observed preponderance of additive effect in spike length. Mohamed[8] and Said[9] also reported similar results for 1000 grain weight. For spike weight, the magnitude of additive effect was higher than dominance gene effects. Dominance x dominance gene effect was found to be significant in the present case.In conclusion, the C scale test showed highly significant values and deviation from zero indicated presence of non- allelic interactions. The mean parameters (*m*) for all studied attributes of the cross (Table 2) indicate that the contribution due to the overall mean plus the locus effects and interaction of the fixed loci was significant. Yield and other related traits exhibited all three types of gene effects i.e. additive, dominance, and epistasis. Hence, for the improvement of the characters additive gene effect can easily be exploited. The epistatic effect (dominance x dominance) was significant for all studied characters which confirm the important role of this gene interaction in the genetic system. This situation in present case would hinder the early selection procedure.

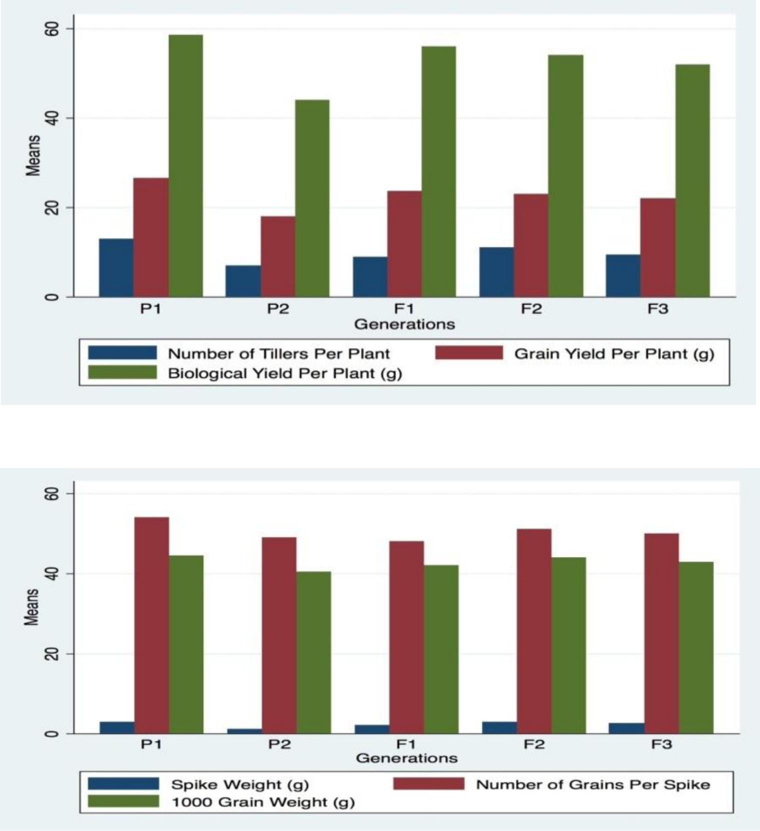

Fig. 1: Means of five generations for different traits in the cross WH1105 X WH711

Table 2: Estimates of C- scaling test and gene effects for all morphological characters in the cross WH1105 X WH711 of wheat

	Plant height	**Number of tillers/ plant**	**Spike length**	**Spike weight**	**Number of grains/spike**	**Number of spikelets/ spike**	**1000 Grain weight**	**Grain yield/ plant 9g)**	**Biological yield/ plant**	**Harvest index**
m	$97.00^{**}\pm0.29$	$11.00^{**}\pm0.43$	$12.00^{**}\pm 0.78$	$2.90^{**}\pm 0.08$	$51.20^{**}\pm 1.19$	$21.00^{**}\pm 0.27$	$44.03^{**}\pm1.71$	$23.00^{**}\pm 0.95$	$54.00^{**}\pm 1.10$	$41.46^{**}\pm 0.56$
d	$2.50^{*}\pm0.39$	$3.00^{**}\pm0.27$	$2.00^{*}\pm0.35$	0.85± 0.05	$2.50^{*}\pm 1.92$	$2.00^{*}\pm 0.63$	$2.06^{**}\pm 1.16$	$3.50^{**}\pm0.95$	$8.00^{**}\pm 1.19$	$2.50^{**}\pm 1.98$
h	1.33±1.06	$2.67^{*}\pm0.94$	1.73 ±0.46	0.33± 0.19	1.07± 1.92	1.33± 0.59	1.65± 1.67	$2.67^{**}\pm 1.11$	$6.67^{**}\pm 1.07$	1.72± 1.34
i	$5.92^{**}\pm1.30$	$6.08^{**}\pm1.21$	$3.62^{**}\pm 0.82$	0.77± 0.24	$5.58^{**}\pm 1.69$	$4.42^{**}\pm 1.49$	$3.14^{**}\pm 1.87$	$6.58^{**}\pm1.77$	$15.08^{**}\pm1.83$	$4.65^{**}\pm1.65$
l	$-10.67^{**}\pm1.37$	$-13.33^{**}\pm 1.68$	$-9.07^{**}\pm 1.79$	$-3.47^{**}\pm 0.74$	$-14.93^{**}\pm1.32$	$-10.67^{**}\pm 1.19$	$-11.01^{**}\pm1.33$	$-5.33^{**}\pm 1.25$	$-5.33^{**}\pm 1.84$	$-5.28^{**}\pm1.00$
Type of epistasis	-	Duplicate	-	-	-	-	-	Duplicate	Duplicate	-
***, **- significant by the t-test at the 5%**	$3.00^{**}\pm1.03$	$6.00^{**}\pm1.02$	$4.80^{**}\pm1.28$	$3.10^{**}\pm 0.44$	$5.80^{**}\pm 1.54$	$4.00^{**}\pm 1.65$	$6.96^{**}\pm 1.80$	$3.00^{**}\pm 1.15$	$4.00^{**}\pm 1.65$	$2.84^{**}\pm 1.53$

***, **- significant by the t-test at the 5% and 1% probability level, respective**

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